

100-443887-100

- (i) APPLICANT: Godowski, Paul J.
Gurney, Austin L.
- (ii) TITLE OF INVENTION: Tie Ligands
- (iii) NUMBER OF SEQUENCES: 17
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Genentech, Inc.
 - (B) STREET: 1 DNA Way
 - (C) CITY: South San Francisco
 - (D) STATE: California
 - (E) COUNTRY: USA
 - (F) ZIP: 94080
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: WinPatin (Genentech)
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Dreger, Ginger R.
 - (B) REGISTRATION NUMBER: 33,055
 - (C) REFERENCE/DOCKET NUMBER: P1130
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 650/225-3216
 - (B) TELEFAX: 650/952-9881

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2290 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

GGCTGAGGGG	AGGCCCGGAG	CCTTTCTGGG	GCCTGGGGGA	TCCTCTTGCA	50
CTGGTGGGTG	GAGAGAAGCG	CCTGCAGCCA	ACCAGGGTCA	GGCTGTGCTC	100
ACAGTTTCCT	CTGGCGGCAT	GTAAAGGCTC	CACAAAGGAG	TTGGGAGTTC	150
AAATGAGGCT	GCTGCGGACG	GCCTGAGGAT	GGACCCCAAG	CCCTGGACCT	200
GCCGAGCGTG	GCACTGAGGC	AGCGGCTGAC	GCTACTGTGA	GGGAAAGAAG	250
GTTGTGAGCA	GCCCCGCAGG	ACCCCTGGCC	AGCCCTGGCC	CCAGCCTCTG	300

CCACTCCAAC CTCAACGGGG TCTGGTACCG CGGGGGCCAT TACCGGAGCC 1900
 GCTACCAGGA CGGAGTCTAC TGGGCTGAGT TCCGAGGAGG CTCTTACTCA 1950
 CTCAAGAAAG TGGTGATGAT GATCCGACCG AACCCCAACA CCTTCCACTA 2000
 AGCCAGCTCC CCCTCCTGAC CTCTCGTGGC CATTGCCAGG AGCCCACCCT 2050
 GGTCACGCTG GCCACAGCAC AAAGAACAAC TCCTCACCAG TTCATCCTGA 2100
 GGCTGGGAGG ACCGGGATGC TGGATTCTGT TTTCCGAAGT CACTGCAGCG 2150
 GATGATGGAA CTGAATCGAT ACGGTGTTTT CTGTCCCTCC TACTTTCCTT 2200
 CACACCAGAC AGCCCCTCAT GTCTCCAGGA CAGGACAGGA CTACAGACAA 2250
 CTCTTTCTTT AAATAAATTA AGTCTCTACA ATAAAAAAA 2290

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Arg	Pro	Leu	Cys	Val	Thr	Cys	Trp	Trp	Leu	Gly	Leu	Leu	Ala	1	5	10	15
Ala	Met	Gly	Ala	Val	Ala	Gly	Gln	Glu	Asp	Gly	Phe	Glu	Gly	Thr	20	25	30	
Glu	Glu	Gly	Ser	Pro	Arg	Glu	Phe	Ile	Tyr	Leu	Asn	Arg	Tyr	Lys	35	40	45	
Arg	Ala	Gly	Glu	Ser	Gln	Asp	Lys	Cys	Thr	Tyr	Thr	Phe	Ile	Val	50	55	60	
Pro	Gln	Gln	Arg	Val	Thr	Gly	Ala	Ile	Cys	Val	Asn	Ser	Lys	Glu	65	70	75	
Pro	Glu	Val	Leu	Leu	Glu	Asn	Arg	Val	His	Lys	Gln	Glu	Leu	Glu	80	85	90	
Leu	Leu	Asn	Asn	Glu	Leu	Leu	Lys	Gln	Lys	Arg	Gln	Ile	Glu	Thr	95	100	105	
Leu	Gln	Gln	Leu	Val	Glu	Val	Asp	Gly	Gly	Ile	Val	Ser	Glu	Val	110	115	120	
Lys	Leu	Leu	Arg	Lys	Glu	Ser	Arg	Asn	Met	Asn	Ser	Arg	Val	Thr	125	130	135	
Gln	Leu	Tyr	Met	Gln	Leu	Leu	His	Glu	Ile	Ile	Arg	Lys	Arg	Asp	140	145	150	
Asn	Ala	Leu	Glu	Leu	Ser	Gln	Leu	Glu	Asn	Arg	Ile	Leu	Asn	Gln	155	160	165	
Thr	Ala	Asp	Met	Leu	Gln	Leu	Ala	Ser	Lys	Tyr	Lys	Asp	Leu	Glu				

				170					175					180
His	Lys	Tyr	Gln	His 185	Leu	Ala	Thr	Leu	Ala 190	His	Asn	Gln	Ser	Glu 195
Ile	Ile	Ala	Gln	Leu 200	Glu	Glu	His	Cys	Gln 205	Arg	Val	Pro	Ser	Ala 210
Arg	Pro	Val	Pro	Gln 215	Pro	Pro	Pro	Ala	Ala 220	Pro	Pro	Arg	Val	Tyr 225
Gln	Pro	Pro	Thr	Tyr 230	Asn	Arg	Ile	Ile	Asn 235	Gln	Ile	Ser	Thr	Asn 240
Glu	Ile	Gln	Ser	Asp 245	Gln	Asn	Leu	Lys	Val 250	Leu	Pro	Pro	Pro	Leu 255
Pro	Thr	Met	Pro	Thr 260	Leu	Thr	Ser	Leu	Pro 265	Ser	Ser	Thr	Asp	Lys 270
Pro	Ser	Gly	Pro	Trp 275	Arg	Asp	Cys	Leu	Gln 280	Ala	Leu	Glu	Asp	Gly 285
His	Asp	Thr	Ser	Ser 290	Ile	Tyr	Leu	Val	Lys 295	Pro	Glu	Asn	Thr	Asn 300
Arg	Leu	Met	Gln	Val 305	Trp	Cys	Asp	Gln	Arg 310	His	Asp	Pro	Gly	Gly 315
Trp	Thr	Val	Ile	Gln 320	Arg	Arg	Leu	Asp	Gly 325	Ser	Val	Asn	Phe	Phe 330
Arg	Asn	Trp	Glu	Thr 335	Tyr	Lys	Gln	Gly	Phe 340	Gly	Asn	Ile	Asp	Gly 345
Glu	Tyr	Trp	Leu	Gly 350	Leu	Glu	Asn	Ile	Tyr 355	Trp	Leu	Thr	Asn	Gln 360
Gly	Asn	Tyr	Lys	Leu 365	Leu	Val	Thr	Met	Glu 370	Asp	Trp	Ser	Gly	Arg 375
Lys	Val	Phe	Ala	Glu 380	Tyr	Ala	Ser	Phe	Arg 385	Leu	Glu	Pro	Glu	Ser 390
Glu	Tyr	Tyr	Lys	Leu 395	Arg	Leu	Gly	Arg	Tyr 400	His	Gly	Asn	Ala	Gly 405
Asp	Ser	Phe	Thr	Trp 410	His	Asn	Gly	Lys	Gln 415	Phe	Thr	Thr	Leu	Asp 420
Arg	Asp	His	Asp	Val 425	Tyr	Thr	Gly	Asn	Cys 430	Ala	His	Tyr	Gln	Lys 435
Gly	Gly	Trp	Trp	Tyr 440	Asn	Ala	Cys	Ala	His 445	Ser	Asn	Leu	Asn	Gly 450
Val	Trp	Tyr	Arg	Gly 455	Gly	His	Tyr	Arg	Ser 460	Arg	Tyr	Gln	Asp	Gly 465
Val	Tyr	Trp	Ala	Glu 470	Phe	Arg	Gly	Gly	Ser 475	Tyr	Ser	Leu	Lys	Lys 480

Val Val Met Met Ile Arg Pro Asn Pro Asn Thr Phe His
485 490 493

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3355 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCAGCTGGTT ACTGCATTTC TCCATGTGGC AGACAGAGCA AAGCCACAAC 50
GCTTTCTCTG CTGGATTAAA GACGGCCAC AGACCAGAAC TTCCACTATA 100
CTACTTAAAA TTACATAGGT GGCTTGTC AAATTCAATTGA TTAGTATTGT 150
AAAAGGAAAA AGAAGTTCCT TCTTACAGCT TGGATTCAAC GGTCCAAAAC 200
AAAAATGCAG CTGCCATTAA AGTCTCAGAT GAACAAACTT CTACACTGAT 250
TTTTTAAAATC AAGAATAAGG GCAGCAAGTT TCTGGATTCA CTGAATCAAC 300
AGACACAAAA AGCTGGCAAT ATAGCAACTA TGAAGAGAAA AGCTACTAAT 350
AAAATTAACC CAACGCATAG AAGACTTTTT TTTCTCTTCT AAAAACAACT 400
AAGTAAAGAC TTAAATTTAA ACACATCATT TTACAACCTC ATTTCAAAAT 450
GAAGACTTTT ACCTGGACCC TAGGTGTGCT ATTCTTCCTA CTAGTGGACA 500
CTGGACATTG CAGAGGTGGA CAATTCAAAA TTAAAAAAT AAACCAGAGA 550
AGATACCCTC GTGCCACAGA TGGTAAAGAG GAAGCAAAGA AATGTGCATA 600
CACATTCCTG GTACCTGAAC AAAGAATAAC AGGGCCAATC TGTGTCAACA 650
CCAAGGGGCA AGATGCAAGT ACCATTAAAG ACATGATCAC CAGGATGGAC 700
CTTGAAAACC TGAAGGATGT GCTCTCCAGG CAGAAGCGGG AGATAGATGT 750
TCTGCAACTG GTGGTGGATG TAGATGGAAA CATTGTGAAT GAGGTAAAGC 800
TGCTGAGAAA GGAAAGCCGT AACATGAACT CTCGTGTTAC TCAACTCTAT 850
ATGCAATTAT TACATGAGAT TATCCGTAAG AGGGATAATT CACTTGAACT 900
TTCCCAACTG GAAAACAAAA TCCTCAATGT CACCACAGAA ATGTTGAAGA 950
TGGCAACAAG ATACAGGGAA CTAGAGGTGA AATACGCTTC CTTGACTGAT 1000
CTTGTCAATA ACCAATCTGT GATGATCACT TTGTTGGAAG AACAGTGCTT 1050
GAGGATATTT TCCCGACAAG ACACCCATGT GTCTCCCCCA CTTGTCCAGG 1100
TGGTGCCACA ACATATTCCT AACAGCCAAC AGTATACTCC TGGTCTGCTG 1150
GGAGGTAACG AGATTCAGAG GGATCCAGGT TATCCCAGAG ATTTAATGCC 1200

ACCACCTGAT CTGGCAACTT CTCCCACCAA AAGCCCTTTC AAGATACCAC 1250
 CGGTAAC TTT CATCAATGAA GGACCATTC AAGACTGTCA GCAAGCAAAA 1300
 GAAGCTGGGC ATTCGGTCAG TGGGATTTAT ATGATTAAAC CTGAAAACAG 1350
 CAATGGACCA ATGCAGTTAT GGTGTGAAAA CAGTTTGGAC CCTGGGGGTT 1400
 GGACTGTTAT TCAGAAAAGA ACAGACGGCT CTGTCAACTT CTTCAGAAAT 1450
 TGGGAAAATT ATAAGAAAGG GTTTGGAAAC ATTGACGGAG AATACTGGCT 1500
 TGGACTGGAA AATATCTATA TGCTTAGCAA TCAAGATAAT TACAAGTTAT 1550
 TGATTGAATT AGAAGACTGG AGTGATAAAA AAGTCTATGC AGAATACAGC 1600
 AGCTTTCGTC TGGAACCTGA AAGTGAATTC TATAGACTGC GCCTGGGAAC 1650
 TTACCAGGGA AATGCAGGGG ATTCTATGAT GTGGCATAAT GGTAACAAT 1700
 TCACCACACT GGACAGAGAT AAAGATATGT ATGCAGGAAA CTGCGCCAC 1750
 TTTCATAAAG GAGGCTGGTG GTACAATGCC TGTGCACATT CTAACCTAAA 1800
 TGGAGTATGG TACAGAGGAG GCCATTACAG AAGCAAGCAC CAAGATGGAA 1850
 TTTTCTGGGC CGAATACAGA GGCGGGTCAT ACTCCTTAAG AGCAGTTCAG 1900
 ATGATGATCA AGCCTATTGA CTGAAGAGAG ACACTCGCCA ATTTAAATGA 1950
 CACAGAACTT TGTACTTTTC AGCTCTTAAA AATGTAAATG TTACATGTAT 2000
 ATTACTTGGC ACAATTTATT TCTACACAGA AAGTTTTTAA AATGAATTTT 2050
 ACCGTAAC TAAGAGGGAA CCTATAAATG TAGTTTCATC TGTCGTCAAT 2100
 TACTGCAGAA AATTATGTGT ATCCACAACC TAGTTATTTT AAAAATTATG 2150
 TTGACTAAAT ACAAAGTTTG TTTTCTAAAA TGTAATATT TGCCACAATG 2200
 TAAAGCAAAT CTTAGCTATA TTTTAAATCA TAAATAACAT GTTCAAGATA 2250
 CTTAACAATT TATTTAAAAT CTAAGATTGC TCTAACGTCT AGTGAAAAAA 2300
 ATATTTTTTA AATTCAGCC AAATAATGCA TTTTATTTTA TAAAAATACA 2350
 GACAGAAAAT TAGGGAGAAA CTTCTAGTTT TGCCAATAGA AAATGTTCTT 2400
 CCATTGAATA AAAGTTATTT CAAATTGAAT TTGTGCCTTT CACACGTAAT 2450
 GATTAAATCT GAATTCTTAA TAATATATCC TATGCTGATT TTCCCAAAC 2500
 ATGACCCATA GTATTAAATA CATATCATTT TTAAAAATAA AAAAAACCC 2550
 AAAAATAATG CATGCATAAT TTAAATGGTC AATTTATAAA GACAAATCTA 2600
 TGAATGAATT TTTCAGTGTT ATCTTCATAT GATATGCTGA ACACCAAAT 2650
 CTCCAGAAAT GCATTTTATG TAGTTCTAAA ATCAGCAAAA TATTGGTATT 2700
 ACAAAAATGC AGAATATTTA GTGTGCTACA GATCTGAATT ATAGTTCTAA 2750

TTTATTATTA CTTTTTTTCT AATTTACTGA TCTTACTACT ACAAAGAAAA 2800
 AAAAACCCTAA CCCATCTGCA ATTCAAATCA GAAAGTTTGG ACAGCTTTAC 2850
 AAGTATTAGT GCATGCTCAG AACAGGTGGG ACTAAAACAA ACTCAAGGAA 2900
 CTGTTGGCTG TTTTCCCGAT ACTGAGAATT CAACAGCTCC AGAGCAGAAG 2950
 CCACAGGGGC ATAGCTTAGT CCAAACCTGCT AATTTTCATTT TACAGTGTAT 3000
 GTAACGCTTA GTCTCACAGT GTCTTTAACT CATCTTTGCA ATCAACAAC 3050
 TTACTAGTGA CTTTCTGGAA CAATTTTCCTT TCAGGAATAC ATATTCAC 3100
 CTTAGAGGTG ACCTTGCCTT AATATATTTG TGAAGTTAAA ATTTTAAAGA 3150
 TAGCTCATGA AACTTTTGCT TAAGCAAAAA GAAACCTCG AATTGAAATG 3200
 TGTGAGGCAA ACTATGCATG GGAATAGCTT AATGTGAAGA TAATCATTTG 3250
 GACAACTCAA ATCCATCAAC ATGACCAATG TTTTTCATCT GCCACATCTC 3300
 AAAATAAAAC TTCTGGTGAA ACAAATTAAA CAAAATATCC AAACCTCAAA 3350
 AAAAA 3355

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 491 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Lys	Thr	Phe	Thr	Trp	Thr	Leu	Gly	Val	Leu	Phe	Phe	Leu	Leu	1	5	10	15
Val	Asp	Thr	Gly	His	Cys	Arg	Gly	Gly	Gln	Phe	Lys	Ile	Lys	Lys	20	25	30	
Ile	Asn	Gln	Arg	Arg	Tyr	Pro	Arg	Ala	Thr	Asp	Gly	Lys	Glu	Glu	35	40	45	
Ala	Lys	Lys	Cys	Ala	Tyr	Thr	Phe	Leu	Val	Pro	Glu	Gln	Arg	Ile	50	55	60	
Thr	Gly	Pro	Ile	Cys	Val	Asn	Thr	Lys	Gly	Gln	Asp	Ala	Ser	Thr	65	70	75	
Ile	Lys	Asp	Met	Ile	Thr	Arg	Met	Asp	Leu	Glu	Asn	Leu	Lys	Asp	80	85	90	
Val	Leu	Ser	Arg	Gln	Lys	Arg	Glu	Ile	Asp	Val	Leu	Gln	Leu	Val	95	100	105	
Val	Asp	Val	Asp	Gly	Asn	Ile	Val	Asn	Glu	Val	Lys	Leu	Leu	Arg	110	115	120	
Lys	Glu	Ser	Arg	Asn	Met	Asn	Ser	Arg	Val	Thr	Gln	Leu	Tyr	Met	125	130	135	

	440		445		450
Asn Gly Val Trp Tyr Arg Gly Gly His Tyr Arg Ser Lys His Gln					
	455		460		465
Asp Gly Ile Phe Trp Ala Glu Tyr Arg Gly Gly Ser Tyr Ser Leu					
	470		475		480
Arg Ala Val Gln Met Met Ile Lys Pro Ile Asp					
	485		490 491		

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1780 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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GGCTCAGAGG CCCCACTGGA CCCTCGGCTC TTCCTTGGAC TTCTTGTTGTG 50
TTCTGTGAGC TTCGCTGGAT TCAGGGTCTT GGGCATCAGA GGTGAGAGGG 100
TGGGAAGGTC CGCCGCGATG GGAAGCCCT GGCTGCGTGC GCTACAGCTG 150
CTGCTCCTGC TGGGCGCGTC GTGGGCGCGG GCGGGCGCCC CGCGCTGCAC 200
CTACACCTTC GTGCTGCCCC CGCAGAAGTT CACGGGCGCT GTGTGCTGGA 250
GCGGCCCCGC ATCCACGCGG GCGACGCCCG AGGCCGCCAA CGCCAGCGAG 300
CTGGCGGCGC TGCGCATGCG CGTCGGCCGC CACGAGGAGC TGTTACGCGA 350
GCTGCAGAGG CTGGCGGCGG CCGACGGCGC CGTGGCCGGC GAGGTGCGCG 400
CGCTGCGCAA GGAGAGCCGC GGCCTGAGCG CGCGCCTGGG CCAGTTGCGC 450
GCGCAGCTGC AGCACGAGGC GGGGCCCGGG GCGGGCCCGG GGGCGGATCT 500
GGGGGCGGAG CCTGCCGCGG CGCTGGCGCT GCTCGGGGAG CGCGTGCTCA 550
ACGCGTCCGC CGAGGCTCAG CGCGCAGCCG CCCGGTTCCA CCAGCTGGAC 600
GTCAAGTTCC GCGAGCTGGC GCAGCTCGTC ACCCAGCAGA GCAGTCTCAT 650
CGCCCGCCTG GAGCGCCTGT GCCCGGGAGG CGCGGGCGGG CAGCAGCAGG 700
TCCTGCCGCC ACCCCCACTG GTGCCTGTGG TTCCGGTCCG TCTTGTGGGT 750
AGCACCAGTG ACACCAGTAG GATGCTGGAC CCAGCCCCAG AGCCCCAGAG 800
AGACCAGACC CAGAGACAGC AGGAGCCCAT GGCTTCTCCC ATGCCTGCAG 850
GTCACCCTGC GGTCCCCACC AAGCCTGTGG GCCCGTGGCA GGATTGTGCA 900
GAGGCCCGCC AGGCAGGCCA TGAACAGAGT GGAGTGTATG AACTGCGAGT 950
GGGCCGTCAC GTAGTGTCAG TATGGTGTGA GCAGCAACTG GAGGGTGGAG 1000

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GCTGGACTGT	GATCCAGCGG	AGGCAAGATG	G TTCAGTCAA	CTTCTTCACT	1050
ACCTGGCAGC	ACTATAAGGC	GGGCTTTGGG	CGGCCAGACG	GAGAATACTG	1100
GCTGGGCCTT	GAACCCGTGT	ATCAGCTGAC	CAGCCGTGGG	GACCATGAGC	1150
TGCTGGTTCT	CCTGGAGGAC	TGGGGGGGCC	GTGGAGCACG	TGCCC ACTAT	1200
GATGGCTTCT	CCCTGGAACC	CGAGAGCGAC	CACTACCGCC	TGCGGCTTGG	1250
CCAGTACCAT	GGTGATGCTG	GAGACTCTCT	TTCCTGGCAC	AATGACAAGC	1300
CCTTCAGCAC	CGTGGATAGG	GACCGAGACT	CCTATTCTGG	TA ACTGTGCC	1350
CTGTACCAGC	GGGGAGGCTG	GTGGTACCAT	GCCTGTGCCC	ACTCCAACCT	1400
CAACGGTGTG	TGGCACCACG	GCGGCCACTA	CCGAAGCCGC	TACCAGGATG	1450
GTGTCTACTG	GGCTGAGTTT	CGTGGTGGGG	CATATTCTCT	CAGGAAGGCC	1500
GCCATGCTCA	TTCGGCCCCT	GAAGCTGTGA	CTCTGTGTTC	CTCTGTCCCC	1550
TAGGCCCTAG	AGGACATTGG	TCAGCAGGAG	CCCAAGTTGT	TCTGGCCACA	1600
CCTTCTTTGT	GGCTCAGTGC	CAATGTGTCC	CACAGAACTT	CCC ACTGTGG	1650
ATCTGTGACC	CTGGGCGCTG	AAAATGGGAC	CCAGGAATCC	CCCCCGTCAA	1700
TATCTTGGCC	TCAGATGGCT	CCCCAAGGTC	ATTCATATCT	CGGTTTGAGC	1750
TCATATCTTA	TAATAACACA	AAGTAGCCAC	1780		

(2) INFORMATION FOR SEO ID NO:6:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Arg	Leu	Gly	Gln	Leu 110	Arg	Ala	Gln	Leu	Gln 115	His	Glu	Ala	Gly	Pro 120
Gly	Ala	Gly	Pro	Gly 125	Ala	Asp	Leu	Gly	Ala 130	Glu	Pro	Ala	Ala	Ala 135
Leu	Ala	Leu	Leu	Gly 140	Glu	Arg	Val	Leu	Asn 145	Ala	Ser	Ala	Glu	Ala 150
Gln	Arg	Ala	Ala	Ala 155	Arg	Phe	His	Gln	Leu 160	Asp	Val	Lys	Phe	Arg 165
Glu	Leu	Ala	Gln	Leu 170	Val	Thr	Gln	Gln	Ser 175	Ser	Leu	Ile	Ala	Arg 180
Leu	Glu	Arg	Leu	Cys 185	Pro	Gly	Gly	Ala	Gly 190	Gly	Gln	Gln	Gln	Val 195
Leu	Pro	Pro	Pro	Pro 200	Leu	Val	Pro	Val	Val 205	Pro	Val	Arg	Leu	Val 210
Gly	Ser	Thr	Ser	Asp 215	Thr	Ser	Arg	Met	Leu 220	Asp	Pro	Ala	Pro	Glu 225
Pro	Gln	Arg	Asp	Gln 230	Thr	Gln	Arg	Gln	Gln 235	Glu	Pro	Met	Ala	Ser 240
Pro	Met	Pro	Ala	Gly 245	His	Pro	Ala	Val	Pro 250	Thr	Lys	Pro	Val	Gly 255
Pro	Trp	Gln	Asp	Cys 260	Ala	Glu	Ala	Arg	Gln 265	Ala	Gly	His	Glu	Gln 270
Ser	Gly	Val	Tyr	Glu 275	Leu	Arg	Val	Gly	Arg 280	His	Val	Val	Ser	Val 285
Trp	Cys	Glu	Gln	Gln 290	Leu	Glu	Gly	Gly	Gly 295	Trp	Thr	Val	Ile	Gln 300
Arg	Arg	Gln	Asp	Gly 305	Ser	Val	Asn	Phe	Phe 310	Thr	Thr	Trp	Gln	His 315
Tyr	Lys	Ala	Gly	Phe 320	Gly	Arg	Pro	Asp	Gly 325	Glu	Tyr	Trp	Leu	Gly 330
Leu	Glu	Pro	Val	Tyr 335	Gln	Leu	Thr	Ser	Arg 340	Gly	Asp	His	Glu	Leu 345
Leu	Val	Leu	Leu	Glu 350	Asp	Trp	Gly	Gly	Arg 355	Gly	Ala	Arg	Ala	His 360
Tyr	Asp	Gly	Phe	Ser 365	Leu	Glu	Pro	Glu	Ser 370	Asp	His	Tyr	Arg	Leu 375
Arg	Leu	Gly	Gln	Tyr 380	His	Gly	Asp	Ala	Gly 385	Asp	Ser	Leu	Ser	Trp 390
His	Asn	Asp	Lys	Pro 395	Phe	Ser	Thr	Val	Asp 400	Arg	Asp	Arg	Asp	Ser 405
Tyr	Ser	Gly	Asn	Cys	Ala	Leu	Tyr	Gln	Arg	Gly	Gly	Trp	Trp	Tyr

	410		415		420									
His	Ala	Cys	Ala	His	Ser	Asn	Leu	Asn	Gly	Val	Trp	His	His	Gly
	425								430					435
Gly	His	Tyr	Arg	Ser	Arg	Tyr	Gln	Asp	Gly	Val	Tyr	Trp	Ala	Glu
	440								445					450
Phe	Arg	Gly	Gly	Ala	Tyr	Ser	Leu	Arg	Lys	Ala	Ala	Met	Leu	Ile
	455								460					465
Arg	Pro	Leu	Lys	Leu										
	470													

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCTGACGAAC CAAGGCAACT ACAAACTCCT GGT 33

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TGCGGCCGGA CCAGTCCTCC ATGGTCACCA GGAGTTTGTA G 41

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGTGGTGAAC TGCTTGCCGT TGTGCCATGT AAA 33

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CAGGTTATCC CAGAGATTTA ATGCCACCA 29

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TTGGTGGGAG AAGTTGCCAG ATCAGGTGGT GGCA 34

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TTCACACCAT AACTGCATTG GTCCA 25

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ACGTAGTTCC AGTATGGTGT GAGCAGCAAC TGGA 34

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AGTCCAGCCT CCACCCTCCA GTTGCT 26

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCCCAGTCCT CCAGGAGAAC CAGCA 25

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2042 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GCGGACGCGT GGGTGAAATT GAAAATCAAG ATAAAAATGT TCACAATTAA 50
GCTCCTTCTT TTTATTGTTC CTCTAGTTAT TTCCTCCAGA ATTGATCAAG 100
ACAATTCATC ATTTGATTCT CTATCTCCAG AGCCAAAATC AAGATTGCT 150
ATGTTAGACG ATGTAAAAAT TTTAGCCAAT GGCCTCCTTC AGTTGGGACA 200
TGGTCTTAAA GACTTTGTCC ATAAGACGAA GGGCCAAATT AATGACATAT 250
TTCAAAAAC TCAACATATTT GATCAGTCTT TTTATGATCT ATCGCTGCAA 300
ACCAGTGAAA TCAAAGAAGA AGAAAAGGAA CTGAGAAGAA CTACATATAA 350
ACTACAAGTC AAAAATGAAG AGGTAAAGAA TATGTCACTT GAACTCAACT 400
CAAAACTTGA AAGCCTCCTA GAAGAAAAAA TTCTACTTCA ACAAAAAGTG 450
AAATATTTAG AAGAGCAACT AACTAACTTA ATTCAAAATC AACCTGAAAC 500
TCCAGAACAC CCAGAAGTAA CTTCACTTAA AACTTTTGTA GAAAAACAAG 550
ATAATAGCAT CAAAGACCTT CTCCAGACCG TGGAAGACCA ATATAAACAA 600
TTAAACCAAC AGCATAGTCA AATAAAAGAA ATAGAAAATC AGCTCAGAAG 650
GACTAGTATT CAAGAACCCA CAGAAATTTT TCTATCTTCC AAGCCAAGAG 700
CACCAAGAAC TACTCCCTTT CTTCACTTGA ATGAAATAAG AAATGTAAAA 750
CATGATGGCA TTCCTGCTGA ATGTACCACC ATTTATAACA GAGGTGAACA 800
TACAAGTGGC ATGTATGCCA TCAGACCCAG CAACTCTCAA GTTTTTCATG 850
TCTACTGTGA TGTTATATCA GGTAGTCCAT GGACATTAAT TCAACATCGA 900
ATAGATGGAT CACAAAACCT CAATGAAACG TGGGAGAACT ACAAATATGG 950
TTTTGGGAGG CTTGATGGAG AATTTTGGTT GGGCCTAGAG AAGATATACT 1000
CCATAGTGAA GCAATCTAAT TATGTTTTAC GAATTGAGTT GGAAGACTGG 1050

AAAGACAACA AACATTATAT TGAATATTCT TTTTACTTGG GAAATCACGA 1100
 AACCAACTAT ACGCTACATC TAGTTGCGAT TACTGGCAAT GTCCCCAATG 1150
 CAATCCCGGA AAACAAAGAT TTGGTGTTTT CTACTTGGGA TCACAAAGCA 1200
 AAAGGACACT TCAACTGTCC AGAGGGTTAT TCAGGAGGCT GGTGGTGGCA 1250
 TGATGAGTGT GGAGAAAACA ACCTAAATGG TAAATATAAC AAACCAAGAG 1300
 CAAAATCTAA GCCAGAGAGG AGAAGAGGAT TATCTTGGAA GTCTCAAAAT 1350
 GGAAGGTTAT ACTCTATAAA ATCAACCAAA ATGTTGATCC ATCCAACAGA 1400
 TTCAGAAAGC TTTGAATGAA CTGAGGCAAT TTAAAGGCAT ATTTAACCAT 1450
 TAACTCATTC CAAGTTAATG TGGTCTAATA ATCTGGTATA AATCCTTAAG 1500
 AGAAAGCTTG AGAAATAGAT TTTTTTTATC TTAAAGTCAC TGTCTATTTA 1550
 AGATTAAACA TACAATCACA TAACCTTAAA GAATACCGTT TACATTTCTC 1600
 AATCAAAATT CTTATAATAC TATTTGTTTT AAATTTTGTG ATGTGGGAAT 1650
 CAATTTTAGA TGGTCACAAT CTAGATTATA ATCAATAGGT GAACTTATTA 1700
 AATAACTTTT CTAAATAAAA AATTTAGAGA CTTTATTTT AAAAGGCATC 1750
 ATATGAGCTA ATATCACAAC TTTCCAGTT TAAAAACTA GTACTCTTGT 1800
 TAAACTCTA AACTTGACTA AATACAGAGG ACTGGTAATT GTACAGTTCT 1850
 TAAATGTTGT AGTATTAATT TCAAACTAA AAATCGTCAG CACAGAGTAT 1900
 GTGTAAAAAT CTGTAATACA AATTTTAAA CTGATGCTTC ATTTTGCTAC 1950
 AAAATAATTT GGAGTAAATG TTTGATATGA TTTATTTATG AAACCTAATG 2000
 AAGCAGAATT AAATACTGTA TTAAAATAAG TTCGCTGTCT TT 2042

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 460 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met	Phe	Thr	Ile	Lys	Leu	Leu	Leu	Phe	Ile	Val	Pro	Leu	Val	Ile
1				5				10						15
Ser	Ser	Arg	Ile	Asp	Gln	Asp	Asn	Ser	Ser	Phe	Asp	Ser	Leu	Ser
				20				25						30
Pro	Glu	Pro	Lys	Ser	Arg	Phe	Ala	Met	Leu	Asp	Asp	Val	Lys	Ile
				35				40						45
Leu	Ala	Asn	Gly	Leu	Leu	Gln	Leu	Gly	His	Gly	Leu	Lys	Asp	Phe
				50				55						60

